



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:02 PM GMT

PDB ID : 1W9B
Title : S. ALBA MYROSINASE IN COMPLEX WITH CARBA-GLUCOTROPAE OLIN
Authors : Bourderioux, A.; Lefoix, M.; Gueyrard, D.; Tatibouet, A.; Cottaz, S.; Arzt, S.; Burmeister, W.P.; Rollin, P.
Deposited on : 2004-10-08
Resolution : 1.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

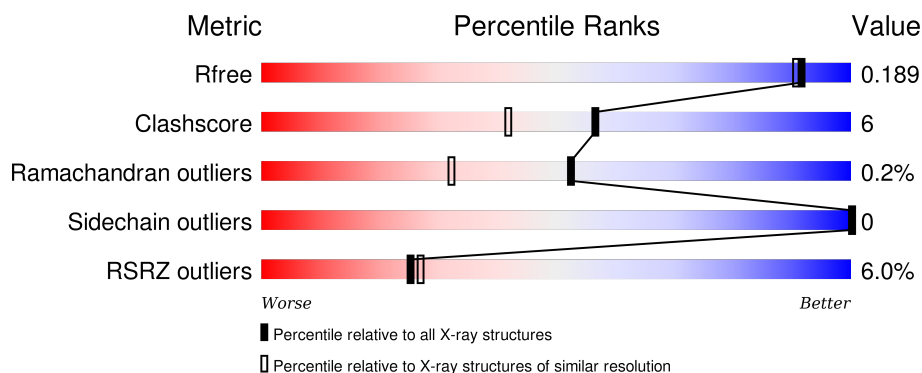
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3190 (1.70-1.70)
Clashscore	102246	3585 (1.70-1.70)
Ramachandran outliers	100387	3527 (1.70-1.70)
Sidechain outliers	100360	3527 (1.70-1.70)
RSRZ outliers	91569	3200 (1.70-1.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	M	501	<div> <div>6%</div> <div>90%</div> <div>10%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	CGT	M	999	-	-	X	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	GOL	M	1000	-	-	X	X
7	GOL	M	1512	-	X	-	X
7	GOL	M	1513	-	X	-	X
9	SO4	M	1503	-	-	-	X

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 5133 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called GLYCOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	M	499	Total	C	N	O	S	0	1	0
			4025	2576	660	773	16			

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	M	1	Total	C	N	O	0	0
			14	8	1	5		
2	M	1	Total	C	N	O	0	0
			14	8	1	5		
2	M	1	Total	C	N	O	0	0
			14	8	1	5		
2	M	1	Total	C	N	O	0	0
			15	8	1	6		
2	M	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	M	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	M	2	Total	C	N	O	0	0
			28	16	2	10		
3	M	2	Total	C	N	O	0	0
			28	16	2	10		

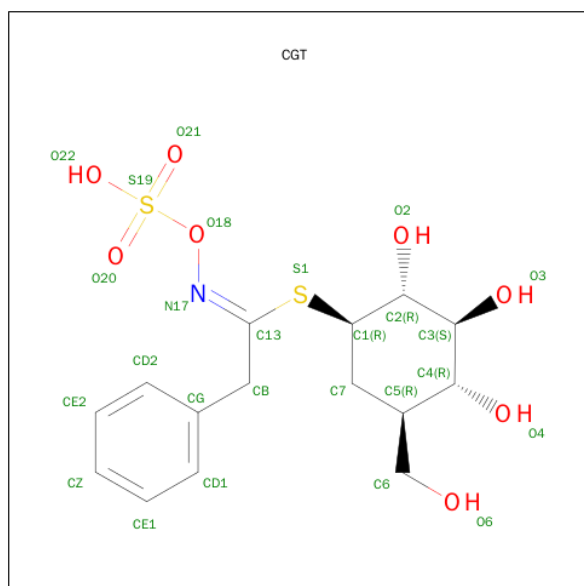
- Molecule 4 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	M	5	Total	C	N	O	0	0
			58	33	2	23		

- Molecule 5 is a polymer of unknown type called SUGAR (7-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	M	7	Total	C	N	O	0	0
			80	45	2	33		

- Molecule 6 is CARBA-GLUCOTROPAEOLIN (three-letter code: CGT) (formula: $C_{15}H_{21}NO_8S_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	M	1	Total	C	N	O	S	0	0
			26	15	1	8	2		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	M	1	Total	C	O	0	0
			6	3	3		
7	M	1	Total	C	O	0	0
			6	3	3		
7	M	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	M	1	Total	Zn	0	0
			1	1		

- Molecule 9 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	M	1	Total	O	S	0	0
			5	4	1		
9	M	1	Total	O	S	0	0
			5	4	1		
9	M	1	Total	O	S	0	0
			5	4	1		
9	M	1	Total	O	S	0	0
			5	4	1		

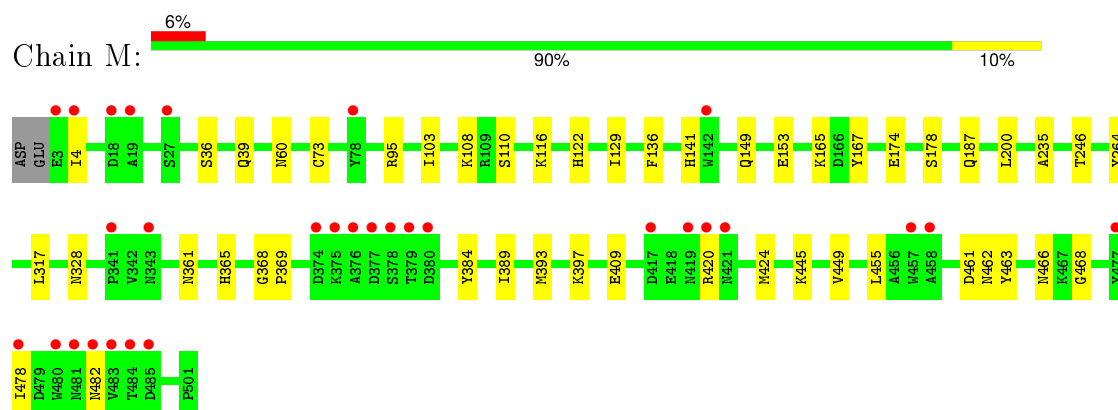
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	M	764	Total	O	0	0
			764	764		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($\text{RSRZ} > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: GLYCOSIDASE



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	135.30Å 137.20Å 80.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	97.00 – 1.70 38.16 – 1.69	Depositor EDS
% Data completeness (in resolution range)	97.4 (97.00-1.70) 96.9 (38.16-1.69)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.30 (at 1.69Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.175 , 0.191 0.191 , 0.189	Depositor DCC
R_{free} test set	4002 reflections (4.98%)	DCC
Wilson B-factor (Å ²)	11.9	Xtriage
Anisotropy	0.090	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 57.2	EDS
Estimated twinning fraction	0.014 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 82050 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5133	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.25% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: XYP, GOL, ZN, BMA, NAG, SO4, MAN, CGT, FUC

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	M	0.31	0/4146	0.60	0/5636

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	M	4025	0	3777	35	0
2	M	85	0	80	8	0
3	M	56	0	50	0	0
4	M	58	0	50	0	0
5	M	80	0	68	2	0
6	M	26	0	18	13	0
7	M	18	0	14	6	0
8	M	1	0	0	0	0
9	M	20	0	0	0	0
10	M	764	0	0	14	0
All	All	5133	0	4057	51	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (51) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:M:999:CGT:C2	7:M:1000:GOL:H32	1.61	1.26
6:M:999:CGT:C2	7:M:1000:GOL:C3	2.19	1.18
6:M:999:CGT:O2	7:M:1000:GOL:H32	1.40	1.17
6:M:999:CGT:H2	7:M:1000:GOL:C3	1.71	1.17
6:M:999:CGT:H7C2	10:M:2739:HOH:O	1.00	1.15
6:M:999:CGT:H2	7:M:1000:GOL:H31	1.33	1.08
6:M:999:CGT:H6C2	10:M:2636:HOH:O	1.69	0.93
1:M:165:LYS:NZ	2:M:931:NAG:H81	1.96	0.80
5:M:954:BMA:H61	10:M:2711:HOH:O	1.83	0.78
1:M:246:THR:HG22	10:M:2374:HOH:O	1.83	0.76
1:M:165:LYS:HZ1	2:M:931:NAG:H81	1.56	0.69
1:M:4:ILE:HD11	1:M:445:LYS:HD2	1.77	0.65
1:M:60:ASN:ND2	2:M:961:NAG:H1	2.13	0.63
2:M:971:NAG:H82	10:M:2498:HOH:O	2.01	0.59
6:M:999:CGT:O20	10:M:2741:HOH:O	2.15	0.59
1:M:108:LYS:HE3	1:M:110:SER:OG	2.04	0.57
1:M:165:LYS:NZ	2:M:931:NAG:C8	2.68	0.56
1:M:462:ASN:HB3	10:M:2631:HOH:O	2.06	0.56
6:M:999:CGT:O2	7:M:1000:GOL:C3	2.32	0.55
1:M:461:ASP:O	1:M:478:ILE:HD12	2.06	0.55
6:M:999:CGT:C7	10:M:2739:HOH:O	1.87	0.52
1:M:95:ARG:HB2	1:M:455:LEU:HD13	1.93	0.49
1:M:165:LYS:HZ3	2:M:931:NAG:C8	2.26	0.49
6:M:999:CGT:C6	10:M:2636:HOH:O	2.45	0.47
1:M:463:TYR:CE1	1:M:468:GLY:HA2	2.50	0.47
6:M:999:CGT:H1	6:M:999:CGT:CG	2.45	0.47
1:M:122:HIS:HE1	1:M:174:GLU:O	1.98	0.46
6:M:999:CGT:H7C1	10:M:2636:HOH:O	2.15	0.46
1:M:39:GLN:O	1:M:462:ASN:HB2	2.16	0.46
1:M:365:HIS:HE1	10:M:2527:HOH:O	1.99	0.45
1:M:95:ARG:HA	1:M:136:PHE:O	2.16	0.45
1:M:397:LYS:HD2	1:M:449:VAL:HA	1.98	0.45
1:M:420:ARG:O	1:M:424:MET:HG2	2.17	0.44
1:M:73:CYS:SG	10:M:2631:HOH:O	2.43	0.43
1:M:36:SER:HB2	1:M:141:HIS:CG	2.53	0.43
1:M:235:ALA:HB1	1:M:317:LEU:HG	2.01	0.43
1:M:95:ARG:NH1	1:M:409:GLU:HG3	2.34	0.42
1:M:482:ASN:HD22	2:M:991:NAG:H82	1.84	0.42
1:M:482:ASN:ND2	2:M:991:NAG:H82	2.35	0.42
1:M:103:ILE:HD11	1:M:167:TYR:CE1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:389:ILE:O	1:M:393:MET:HG2	2.20	0.42
1:M:129:ILE:CD1	1:M:178:SER:HB3	2.50	0.42
1:M:368:GLY:HA3	1:M:384:TYR:O	2.20	0.41
5:M:956:MAN:H61	10:M:2434:HOH:O	2.20	0.41
1:M:4:ILE:CD1	1:M:445:LYS:HD2	2.49	0.41
1:M:328:ASN:CG	1:M:409:GLU:HB2	2.39	0.41
1:M:116:LYS:HG2	10:M:2240:HOH:O	2.20	0.41
1:M:369:PRO:HB2	1:M:384:TYR:CE2	2.56	0.40
1:M:264:TYR:O	1:M:361:ASN:HB2	2.21	0.40
1:M:149:GLN:O	1:M:153:GLU:HA	2.21	0.40
1:M:200:LEU:O	1:M:466:ASN:ND2	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	M	498/501 (99%)	480 (96%)	17 (3%)	1 (0%)	52 32

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	M	187	GLN

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	436/437 (100%)	436 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	M	122	HIS
1	M	365	HIS
1	M	398	ASN
1	M	462	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

16 carbohydrates are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	M	921	1,3	14,14,15	0.42	0	15,19,21	0.68	1 (6%)
3	NAG	M	923	3	14,14,15	0.39	0	15,19,21	0.79	1 (6%)
4	NAG	M	941	1,4	14,14,15	0.42	0	15,19,21	0.71	1 (6%)
4	FUC	M	942	4	10,10,11	0.38	0	14,14,16	0.51	0
4	NAG	M	943	4	14,14,15	0.38	0	15,19,21	0.75	1 (6%)
4	BMA	M	944	4	11,11,12	0.30	0	14,15,17	0.31	0
4	XYP	M	945	4	9,9,10	0.44	0	12,12,14	0.51	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	M	951	1,5	14,14,15	0.43	0	15,19,21	0.69	0
5	FUC	M	952	5	10,10,11	0.41	0	14,14,16	0.45	0
5	NAG	M	953	5	14,14,15	0.38	0	15,19,21	0.76	0
5	BMA	M	954	5	11,11,12	0.37	0	14,15,17	0.49	0
5	XYP	M	955	5	9,9,10	0.43	0	12,12,14	0.56	0
5	MAN	M	956	5	11,11,12	0.33	0	14,15,17	0.59	0
5	MAN	M	957	5	11,11,12	0.36	0	14,15,17	0.58	0
3	NAG	M	981	1,3	14,14,15	0.50	0	15,19,21	0.68	0
3	NAG	M	983	3	14,14,15	0.73	0	15,19,21	1.37	1 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	M	921	1,3	-	0/6/23/26	0/1/1/1
3	NAG	M	923	3	-	0/6/23/26	0/1/1/1
4	NAG	M	941	1,4	-	0/6/23/26	0/1/1/1
4	FUC	M	942	4	-	0/0/17/20	0/1/1/1
4	NAG	M	943	4	-	0/6/23/26	0/1/1/1
4	BMA	M	944	4	-	0/2/19/22	0/1/1/1
4	XYP	M	945	4	-	0/0/14/17	0/1/1/1
5	NAG	M	951	1,5	-	0/6/23/26	0/1/1/1
5	FUC	M	952	5	-	0/0/17/20	0/1/1/1
5	NAG	M	953	5	-	0/6/23/26	0/1/1/1
5	BMA	M	954	5	-	0/2/19/22	0/1/1/1
5	XYP	M	955	5	-	0/0/14/17	0/1/1/1
5	MAN	M	956	5	-	0/2/19/22	0/1/1/1
5	MAN	M	957	5	-	0/2/19/22	0/1/1/1
3	NAG	M	981	1,3	-	0/6/23/26	0/1/1/1
3	NAG	M	983	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	M	983	NAG	C2-N2-C7	-4.49	117.27	123.04
3	M	923	NAG	C2-N2-C7	-2.38	119.98	123.04
4	M	943	NAG	C2-N2-C7	-2.31	120.07	123.04
3	M	921	NAG	C2-N2-C7	-2.05	120.40	123.04
4	M	941	NAG	C2-N2-C7	-2.05	120.41	123.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	M	954	BMA	1	0
5	M	956	MAN	1	0

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 1 is monoatomic - leaving 14 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
7	GOL	M	1000	6	5,5,5	0.56	0	5,5,5	1.02	1 (20%)
9	SO4	M	1503	-	4,4,4	0.17	0	6,6,6	0.07	0
9	SO4	M	1504	-	4,4,4	0.23	0	6,6,6	0.08	0
9	SO4	M	1505	-	4,4,4	0.22	0	6,6,6	0.09	0
9	SO4	M	1506	-	4,4,4	0.18	0	6,6,6	0.08	0
7	GOL	M	1512	-	5,5,5	4.86	5 (100%)	5,5,5	5.68	3 (60%)
7	GOL	M	1513	-	5,5,5	4.80	5 (100%)	5,5,5	5.70	3 (60%)
2	NAG	M	901	1	14,14,15	0.38	0	15,19,21	0.74	1 (6%)
2	NAG	M	911	1	14,14,15	0.44	0	15,19,21	0.77	1 (6%)
2	NAG	M	931	1	14,14,15	0.32	0	15,19,21	0.77	1 (6%)
2	NAG	M	961	-	15,15,15	0.31	0	17,21,21	0.56	0
2	NAG	M	971	1	14,14,15	0.41	0	15,19,21	0.73	1 (6%)
2	NAG	M	991	1	14,14,15	0.39	0	15,19,21	0.74	1 (6%)
6	CGT	M	999	1,7	24,27,27	1.01	2 (8%)	22,38,38	1.01	1 (4%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	GOL	M	1000	6	-	0/4/4/4	0/0/0/0
9	SO4	M	1503	-	-	0/0/0/0	0/0/0/0
9	SO4	M	1504	-	-	0/0/0/0	0/0/0/0
9	SO4	M	1505	-	-	0/0/0/0	0/0/0/0
9	SO4	M	1506	-	-	0/0/0/0	0/0/0/0
7	GOL	M	1512	-	-	0/4/4/4	0/0/0/0
7	GOL	M	1513	-	-	0/4/4/4	0/0/0/0
2	NAG	M	901	1	-	0/6/23/26	0/1/1/1
2	NAG	M	911	1	-	0/6/23/26	0/1/1/1
2	NAG	M	931	1	-	0/6/23/26	0/1/1/1
2	NAG	M	961	-	-	0/6/26/26	0/1/1/1
2	NAG	M	971	1	-	0/6/23/26	0/1/1/1
2	NAG	M	991	1	-	0/6/23/26	0/1/1/1
6	CGT	M	999	1,7	-	0/7/36/36	0/2/2/2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	M	1512	GOL	C3-C2	-8.31	1.20	1.52
7	M	1513	GOL	C3-C2	-8.17	1.21	1.52
6	M	999	CGT	O18-S19	-3.50	1.50	1.65
7	M	1512	GOL	O2-C2	-3.33	1.33	1.43
7	M	1513	GOL	C1-C2	-3.14	1.40	1.52
7	M	1513	GOL	O2-C2	-2.94	1.34	1.43
7	M	1512	GOL	C1-C2	-2.93	1.41	1.52
6	M	999	CGT	C7-C1	-2.33	1.49	1.54
7	M	1512	GOL	O3-C3	2.99	1.55	1.42
7	M	1513	GOL	O3-C3	3.19	1.56	1.42
7	M	1513	GOL	O1-C1	4.44	1.61	1.42
7	M	1512	GOL	O1-C1	4.53	1.61	1.42

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	M	999	CGT	C5-C7-C1	-4.09	108.27	113.05
2	M	931	NAG	C2-N2-C7	-2.36	120.00	123.04
2	M	911	NAG	C2-N2-C7	-2.32	120.06	123.04
2	M	991	NAG	C2-N2-C7	-2.26	120.13	123.04
2	M	971	NAG	C2-N2-C7	-2.25	120.15	123.04
2	M	901	NAG	C2-N2-C7	-2.20	120.22	123.04
7	M	1000	GOL	C3-C2-C1	-2.12	102.80	111.12
7	M	1512	GOL	O1-C1-C2	3.23	125.85	110.18
7	M	1513	GOL	O1-C1-C2	3.29	126.12	110.18

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
7	M	1512	GOL	O2-C2-C3	6.39	137.94	108.65
7	M	1513	GOL	O2-C2-C3	6.61	138.96	108.65
7	M	1513	GOL	O3-C3-C2	10.34	160.35	110.18
7	M	1512	GOL	O3-C3-C2	10.46	160.92	110.18

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	M	1000	GOL	6	0
2	M	931	NAG	4	0
2	M	961	NAG	1	0
2	M	971	NAG	1	0
2	M	991	NAG	2	0
6	M	999	CGT	13	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	M	499/501 (99%)	0.18	30 (6%)	25 27	6, 11, 28, 56	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	376	ALA	10.0
1	M	378	SER	5.6
1	M	375	LYS	5.2
1	M	377	ASP	4.9
1	M	417	ASP	4.7
1	M	379	THR	4.6
1	M	458	ALA	4.6
1	M	3	GLU	4.1
1	M	421	ASN	4.0
1	M	483	VAL	3.8
1	M	481	ASN	3.4
1	M	4	ILE	3.3
1	M	485	ASP	3.1
1	M	374	ASP	3.0
1	M	380	ASP	3.0
1	M	343	ASN	2.7
1	M	419	ASN	2.7
1	M	18	ASP	2.7
1	M	477	TYR	2.7
1	M	482	ASN	2.6
1	M	341	PRO	2.5
1	M	420	ARG	2.5
1	M	19	ALA	2.4
1	M	78	TYR	2.3
1	M	27	SER	2.2
1	M	478	ILE	2.2
1	M	457	TRP	2.2

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Mol	Chain	Res	Type	RSRZ
1	M	480	TRP	2.2
1	M	484	THR	2.2
1	M	142	TRP	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	NAG	M	921	14/15	0.94	0.12	0.84	17,22,27,30	0
3	NAG	M	981	14/15	0.96	0.07	-0.53	10,14,15,18	0
4	BMA	M	944	11/12	0.79	0.36	-	45,48,49,50	0
5	NAG	M	951	14/15	0.94	0.10	-	19,22,25,26	0
4	NAG	M	941	14/15	0.94	0.13	-	17,19,23,26	0
5	MAN	M	957	11/12	0.61	0.35	-	53,55,56,56	0
3	NAG	M	923	14/15	0.67	0.43	-	37,40,42,43	0
4	NAG	M	943	14/15	0.86	0.19	-	28,33,39,40	0
5	MAN	M	956	11/12	0.70	0.19	-	43,49,50,50	0
5	XYP	M	955	9/10	0.73	0.24	-	49,49,52,52	0
3	NAG	M	983	14/15	0.69	0.37	-	22,28,34,36	0
4	FUC	M	942	10/11	0.82	0.26	-	30,33,36,38	0
4	XYP	M	945	9/10	0.67	0.47	-	51,52,53,53	0
5	FUC	M	952	10/11	0.90	0.12	-	25,26,30,31	0
5	NAG	M	953	14/15	0.90	0.12	-	24,31,33,36	0
5	BMA	M	954	11/12	0.81	0.19	-	43,46,48,51	0

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
9	SO4	M	1503	5/5	0.97	0.20	15.71	34,36,37,39	0
6	CGT	M	999	26/26	0.83	0.40	13.65	24,30,37,39	26
7	GOL	M	1000	6/6	0.94	0.33	10.59	9,12,14,15	6
7	GOL	M	1512	6/6	0.77	0.24	7.96	18,25,30,34	0
7	GOL	M	1513	6/6	0.83	0.21	6.56	20,30,33,40	0
2	NAG	M	901	14/15	0.83	0.23	1.47	29,33,38,39	0
9	SO4	M	1504	5/5	0.88	0.21	-	40,43,44,44	0
2	NAG	M	931	14/15	0.81	0.29	-	38,42,45,46	0
9	SO4	M	1505	5/5	0.80	0.19	-	67,67,67,67	0
8	ZN	M	1502	1/1	1.00	0.07	-	8,8,8,8	1
2	NAG	M	971	14/15	0.55	0.60	-	50,55,56,57	0
9	SO4	M	1506	5/5	0.99	0.05	-	20,21,24,25	0
2	NAG	M	911	14/15	0.90	0.21	-	22,27,30,32	0
2	NAG	M	961	15/15	0.40	0.70	-	82,82,83,83	0
2	NAG	M	991	14/15	0.37	0.60	-	55,57,60,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.